

FIG.1A

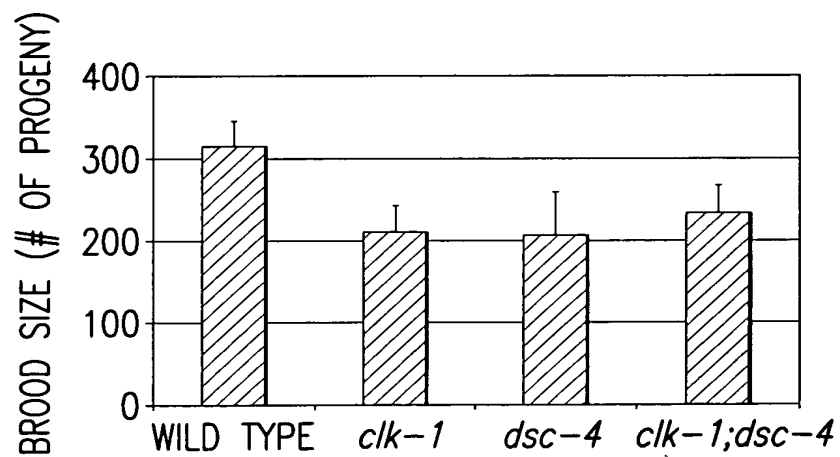


FIG.1B

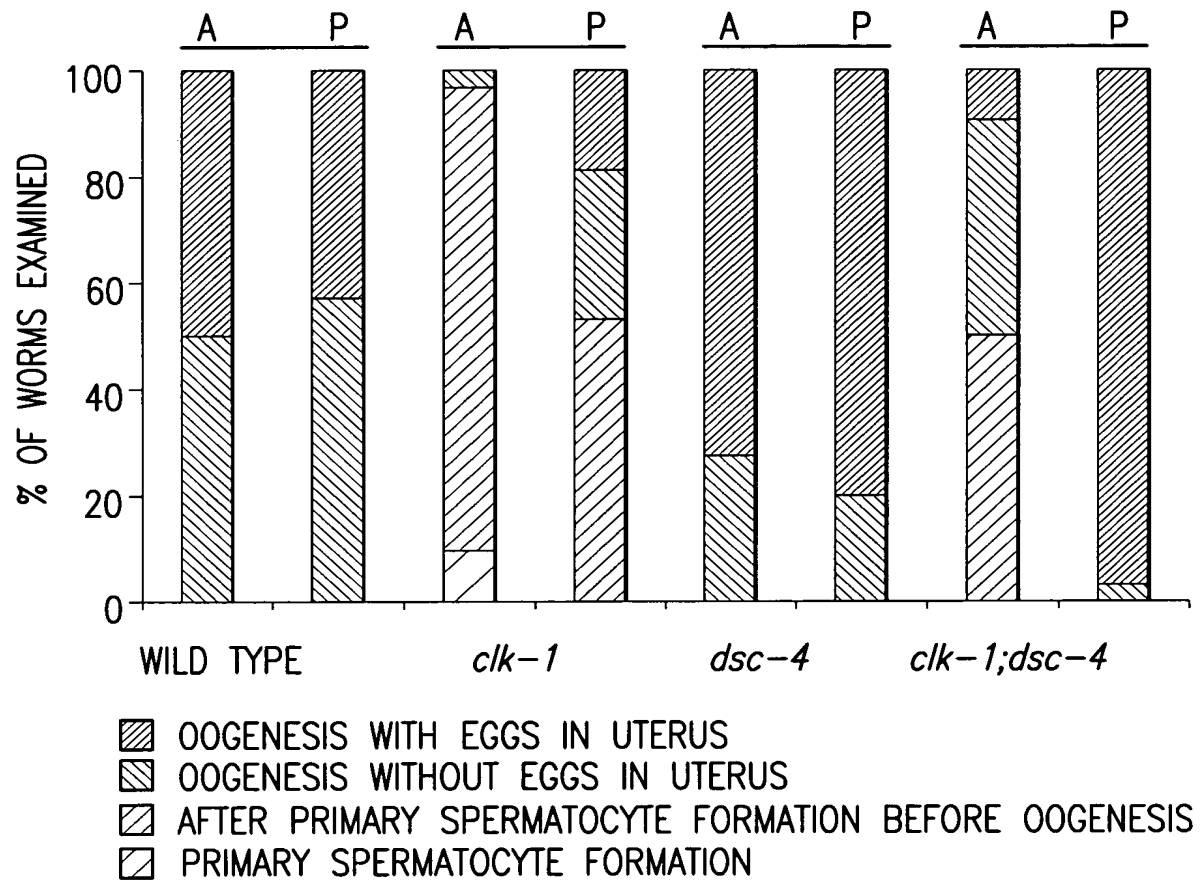


FIG.1C

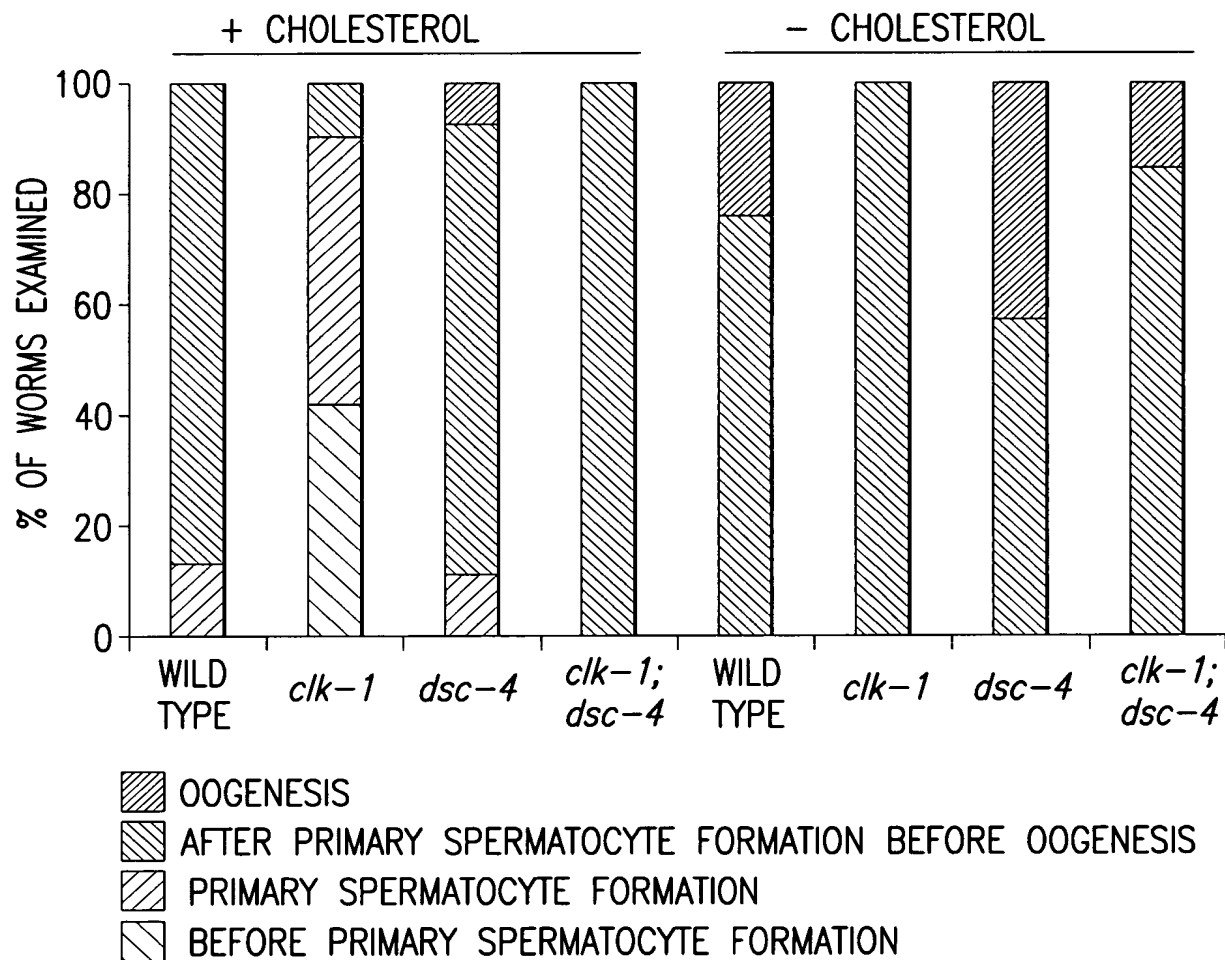


FIG.1D

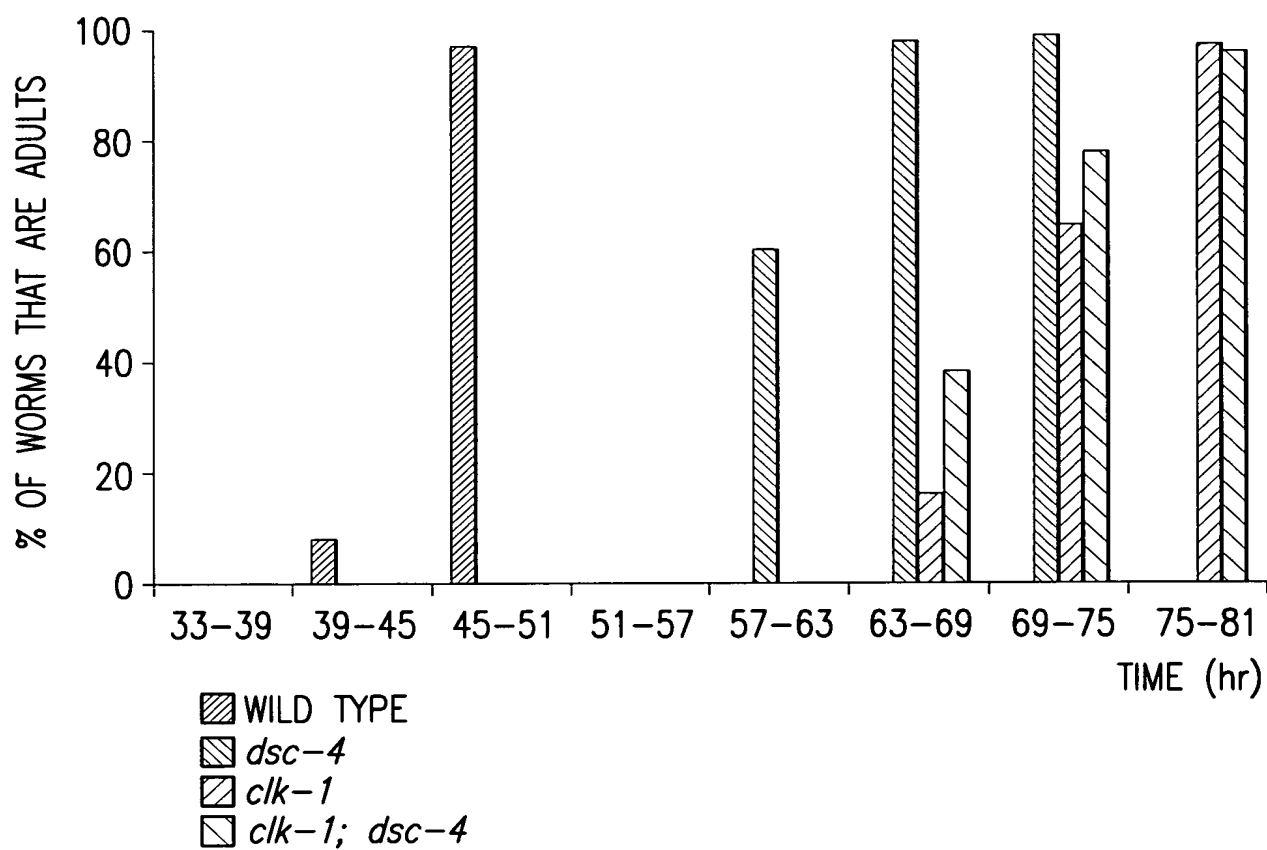


FIG.1E

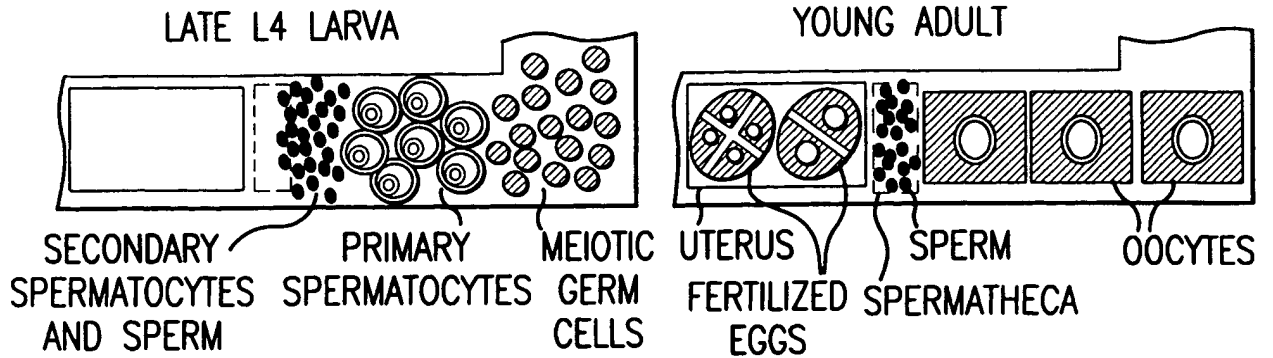


FIG.2A-1

FIG.2A-2

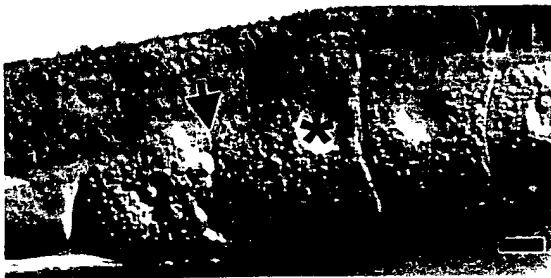


FIG.2B

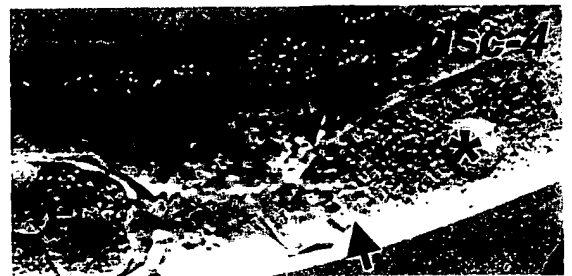


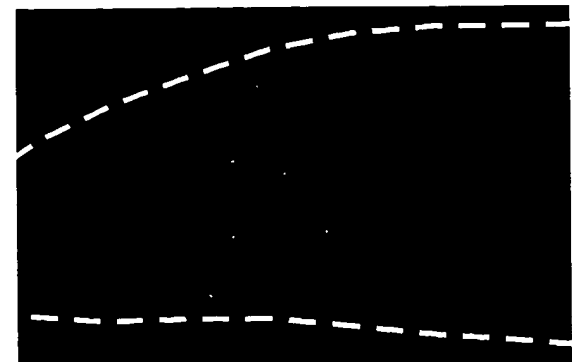
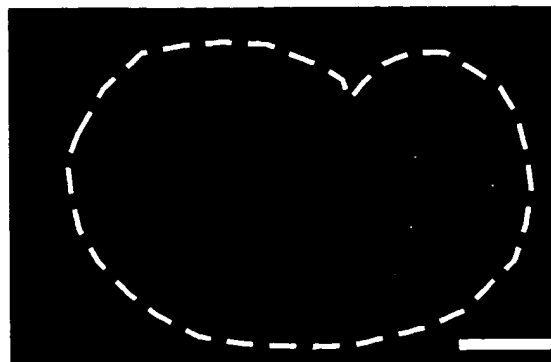
FIG.2C



FIG.2D



FIG.2E



Dsc-4	AVPDLDEIKKNLRKHGPDYYKNQPKMNEIVRLKVDYWFRTESMIYDDIDNKEKDPSTVIAGNFSFETLHHDVEGMLGRFTLT	85
ZebrafishAGPRLDNGKLYRYSYGFEVGNRP TGSPENGVGR ISSD V D I N L A W R N P E I Q D E Q L L Q V Q I S N I Q V E S A G K H	72
MouseVKGHTTGLSLNNERLYKL TYSFEVFDGGK GK PQD SVGYK ISSD V D V L L W R N P D G D D D Q V I Q V T I T A V N V E N A G Q Q	77
HumanVKGHTTGLSLNDRLYKL TYSFEVLDRGK GK LQD SVGYR ISSN V D V A L L W R N P D G D D D Q L I Q I T M K D V N V E N V N Q Q	77
Dsc-4	QCNTDNCGNPPIYIAFR.....QCGNNAEHILKASDES DATW N F L Y A I V X T I Y T P A E Y G E G D E Q T V D T I Y G R C F V N F G R	160
Zebrafish	SRKNNIFHGSAAESLCKVRLEALQRPFLVLWKMGKIRSLYAQKAEPATVKKLRGVASMLMMQLKSGKMSEADASCKQLVEYKVV	157
Mouse	RCEKSIFQKSTPKIIGKDNLEALQRPMLLHLVRGKVKEFYSENEPVGIEKLRGLASLFQMQLSSGTTNEVDISQDCKXYTYQA	162
Human	RGEKSIFGKKSPSKIMGKENLEALQRPRTLHLIHGKVKEFYSYQNEAVAIEKLRGLASLFTQLSSGTTNEVDISQDCKXYTYQA	162
Dsc-4	PEDKRFRRRIIEKCDLGYGTNFKFEGIESVQYQDQVWYIQNTKVDADIIMVDAIEMLAFKSPLEHKYGFLESRTHVEITNRTRV	245
Zebrafish	NKHQVIRTKHLETKSQETGEZTHS.PVLGISGKCAAEIVITLENGIIKSADAKETHVLSINARHKAA TKVL\$RQSL TLKAI EAG	241
Mouse	QDDKVVKIKALDTCKIERSGFTAN.QVLGVSSKATSVZTYKIEDSFVTAVLAEETRAFALNFQQT IAGKIV\$KQKLELKTTEAG	246
Human	HQDKVIKIKALDSCKIARSGFTPN.QVLGVSSKATSVZTYKIEDSFVIAVLAEETHNFGLNFLQTIKGIIV\$KQKLELKTTEAG	246
Dsc-4	FVTSYCN DTVPSAKCAEQAFGAVRVGKLYEHVKIAEQSNKZTKLIGTYRRHIZQDMGDSHICEKHSLSYSQIAQEARLAKRQDW	330
Zebrafish	PAEVAGKDVAGVVKALDDKFLSVGVIVEKTKPKCKG...CPNIMETWKA VRSQZEPNSLSKAEAPRSFZTLVHSLRKSSKSEILT	323
Mouse	PRMIPGKQVAGVTKAVDSKYKAIPIVGQVLERVCKG...CPSZAEHWKSI\$KKNZEPENLSKAEAVQSFZAF IQHLRTSRREEILQ	328
Human	PRLMSGKQAAAIIKAVDSKYTAIPIVGQVFSQSHCKG...CPSZSELWRST\$KYQZQPDNL\$KAEAVRNFAF IQHLRTAKKEEILQ	328
Dsc-4	EAAIQYPENDHVZSLIASALGGVGTAESZTTAREVLLTASPDYLDLZFCISQSSNNZKWHKQZMYWLGLSDKKSEYWKXANT	415
Zebrafish	VLQNCSTALPQZVDAVTSAQTPSSLSAFLFLDFSKKDGILQERFZYACGFASHPTZSMLQSLEVSQKIGSTEIKESXVII	408
Mouse	ILKAEKKEVLPQZVDAVTSAQTPDSLEAFLDFLDFKSDSSIILQERFZYACGFATHPDELLRAFLSKFKGSFASNDIRESXMI	413
Human	ILKMENKEVLPQZVDAVTSAQTSDSLEAFLDFLDFKSDSSIILQERFZYACGFASHPNZELLRAFLSKFKGSIGSSDIRETXMI	413

FIG. 3A-1

Dsc-4	IATVLNRRCEASTSSNSCNKG ETIVNKF ITDLTAGGVEVRV EVLENIP IF CSYTF AK KF ICETESEDVQKAALNVI E AASKN	500
Zebrafish	MGALLR KL LKGACD LPWLVK ELL AGPD STQEESEVQMYL ALKNALLPE IPVL TK YAESEVGA...YSTIAT A QRYDP	490
Mouse	IGALVR KL LQNEGCK KAVE AK KL ILGGLKPEKKEDTMYL ALKNALLPE IPLL LY AEAGECP...VSHLATT V QRYDV	495
Human	TGTLVR KL LQNEGCK KAVE AK KL ILGGLKAEKKEDTRMYL ALKNALLPE IPSL L LYAEAGECP...ISHLATT A QRYDL	495
Dsc-4	LYE Z QLTH K LIKLFRNTCSQETPTSHSQL ADID ILLKCV DD HQN ATL I ERT ET NPDD QEKWHYL YKA IEASGNKDELKAEFWSR	585
Zebrafish	ALI Z AEVK K ALNR IYHQ NQRIYEKNVRA AAAD ADVIMSSN PS YME YKNLL ESIGH EPHEM KYMLSKI QD VLRFQMPAYKLVRQVMK	575
Mouse	SFI Z DEVK K TLNR IYHQ NRKVVHEKTVRTT AA AVILKN. PSYMD K KN IL ES IGEL EPKEM NKYMLTVVQDILHFEMPASKMIRRVLK	579
Human	PF I DEVK K TLNR IYHQ NRKVVHEKTVRTT AA AILNNN PSYMD K KN IL ES IGEL EPQEM NKYMLAIVQDILRLEMPASKI VR RVLK	580
Dsc-4	MRKFKVFRPNFLH R ALQ AD SHVHWQEIADASN FQ ESTANTEFLQSKF KRS FE LSM KKGRKEHNL FS LSIDT EH LEQFVIGSAS	670
Zebrafish	DMISHNYDRFSK TG SS AYSG FMAETVDVTCTYN ED ILYSGSVLRRSNM N YGCNNALLHGLQVTIEA QGL ESPIAATPDEGE	660
Mouse	EMAVHNYDRFSK SG SS AYTG YVERSPRAASTYS ED ILYSGGILRRSNL N FQYIKGTELHGSQVIEA QGL EGLIAATPDEGE	664
Human	EMVAHNYDRFSR SG SS AYTG YIERSPRSASTYS ED ILYSGGILRRSNL N FQYIGKAGLHGSQVIEA QGL EGLIAATPDEGE	665
Dsc-4	SRSGAPQ Q SVRIGVAGHK EP THHIF K ST DL L ST VM EAD ERTHKAFEGHVPVR SV PL SL TLDVDSVGAISMRV LA SA EV	755
Zebrafish	EELESFA Q .MSALLFDVQ LR PVTF EN YSD LM SKMFST S SDPINVK GL ILLT HS QV IP Q SG LRASAEFQAGLSIDISGGM EF	744
Mouse	ENLDSYA Q .MSAILFDVQ LR PVTF EN YSD LM SKMLSAS SD DPVSVK GL ILLT HS QD IQ Q SG LKANMEIQGGLAIDISGSM EF	748
Human	ENLDSYA Q .MSAILFDVQ LR PVTF EN YSD LM SKMLSAS SD DPISVK GL ILLT HS QELQ Q Q SG LKANIEVQGGLAIDISGAM EF	749

FIG.3A-2

Dsc-4
Zebrafish
Mouse
Human

~~SLWYRQ~~. . . NAKAEAYTSCSLHL~~ASLYHHSEPV~~RHVES~~I~~SA~~STFT~~TDTRAIFET~~TPYDFCLRTS~~NSNVDINQ~~KT~~VVQDQICK 838
~~SLWYRES~~KT~~SVNN~~RGALVIIGNM~~VD~~TDFVSAGVEVGFE~~AT~~DFIT~~TVQFSEYPF~~VCMQMDKTTFF~~RE~~TVS~~Q~~EKLPTGQM 829
~~SLWYRES~~KT~~RVKN~~RVAVVITSDV~~VD~~AS~~FKAGLESRAE~~ZEAG~~EFIS~~TVQFSQYPF~~VCMQMDKAEAPLRQFE~~TKYERLSTGRG 833
~~SLWYRES~~KT~~RVKN~~RVVT~~VT~~ITTDI~~VD~~SS~~FKAGLET~~STE~~ZEAG~~EFIS~~TVQFSQYPF~~VCMQMDKDEAP~~FRQFE~~KKYERLSTGRG 834

Dsc-4
Zebrafish
Mouse
Human

HKKKTLNRKRVHP~~Q~~VTYR~~Q~~DDSTIR~~Q~~NSYLEQFRL 874
FSRKRS.RDQVVP~~Q~~SEFF~~P~~HQENS~~M~~KKVFEPAW 863
YVSRRR.KESLVAG~~CEL~~P~~H~~HQENSE~~M~~NNVFPQPESDNSGGWF 876
YVSQKR.KESVLAG~~CEFF~~P~~H~~HQENSE~~M~~KVVFAPQPD~~S~~.TSSGWF 876

FIG. 3A-3

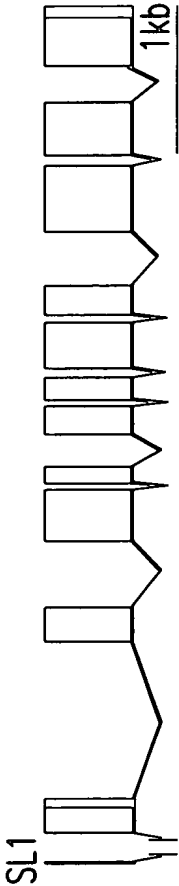


FIG. 3B

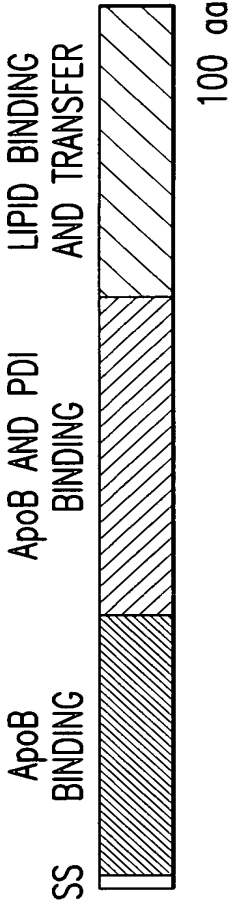


FIG. 3C

1 TTTAATTACCCAAGTTTGAGTGTATCAGCAAGCATAAATCATAACTCTTATCAATAGTACTGCTTCTCTGCAATTCACAAATTCCTCTTCCATCCAAACA

106 G G A C T C C A T T G C C A A T A A A A T T A T T T T G C T C T C T G G G A G A A A T T T G G A A C C A G A G A T G T T C T C A T C A C G G A T A T G G C T G C T T C T G G C G T T A C T G T
1 M F S S R I W L L L A V T V

211 G G G A G T T T G C C T A G C A G T T C C G G A T C T C G A T G A A A T C A G A G A A C C T T C G C A A C A T G G T C C A G A C T A C T A T A A A A T C A G C C G A A A T G A A C G A G A C A C T G T
15 G V C L A V P D L D E I K K N L R K H G P D Y Y K N Q P K M N E N T V

316 C C G A C T A C T G A A A G T G C A T T A C T G G T T C C G T A C T G A A T C T A T G A T T T A C G A T G A T A T T G A T A A T A A G G A G A G G A T C C A T C G A C C G T T A T T G C T G G A A A T T T C A G
50 R L L K V D Y W F R T E S M I Y D D I D N K E K D P S T V I A G N F S

421 C T T T G A A A C A C T T C A T C A G C T G G A G G T G C A T G T T G G A C C G T T T A C C C T A A C C C A A T G C A A C A C T G A C A C T G T G G T A T C C A T C T C C A A T C T A C A T A G C
85 F E T L H H D V E G G M L G R F T L T Q C N T D N C G N P S P I Y I A

526 A T T C C G T C A A G G T G G T A A T A T G C G A G C A T A T C C T T A A A G C G T C C G A T G A G A G T G A C G C C A C C T G G A A T T T C C T G T A C G C A A T T G T G A A T A C A A T C T A C A C C C C
120 F R Q G G N N A E H I L K A S D E S D A T W N F L Y A I V N T I Y T P

631 A G C A G A T A C G G A A G G A C G A G C A A C A G T C G A C A C A A T T T A C G G A A G A T G C T T C G T G A A C T T T G G A A G C C A G A G A T A A A C G G T T T A G A A G A A T T A T C G A
155 A E Y G E G D E Q T V D T I Y G R C F V N F G R P E D K R F R I I E

736 G A A G T G T G A T T T G G G T A C G G C A C A A A T T T T A C G A A A T T C G A A G G A A T C G A G A G T G T T C A A T A T G A T C A G G A T G T C T G G T A C A C A G A C A C A A A A G T C G A T G C
190 K C D L G Y G T N F T K F E G I E S V Q Y D Q D V W Y T Q N T K V D A

841 A G A C A T T A T T A T G T T G A T G T T A G C A T T C A A G A G T C C A C T T C A C G A G A A A T A C G G A T T C A C T C T G G A A T C C A G A A C T C A C G T A G A A A T C A C C A A
225 D I I M V D A I E M L A F K S P L H E K Y G F T L E S R T H V E I T N

FIG. 4A

946 CCGTACACGTGCTTCGTCACCAGCTACTGTAATGATACCGTACCATCCGCCAAATGCGCCGAGCAGCGTTTGGACGAGTTCCGTGTCGGAGGAAACTTTACGA
260 R T R V F V T S Y C N D T V P S A K C A E Q A F G A V R V G G K L Y E

1051 GCATGTCAGATTGCCAGGAACAGTCGAATAAGTTAACAAAGCTTATTGGAAACATACCGCGTCACTCTTCAAGATATGGTGACTCACACATTTTGTGAGAAACA
295 H V K I A Q E Q S N K L T K L I G T Y R R H L Q D M G D S H I C E K H

1156 TTCITTGCTTTATAGTCAAAATTGCTCAAGAAGCCCGATTGGCTAAGCGACAGGACTGGGAAGCTGCTATCCAATACCCAGAGAATGATCAITGTCIATCITAT
330 S L L Y S Q I A Q E A R L A K R Q D W E A A I Q Y P E N D H V L S L I

1261 CGCCAGTCCCTCGGAGGAGTCGGTACAGCAGAATCTATCACCACTCGTCGTAAGTTCTTCTTACCGCTCCCTGATTATCTTGATGATTTACTTTTGGAAAT
365 A S A L G G V G T A E S I T I A R E V L L T A S P D Y L D D L L F G I

1366 TTCACAAAGCTCGCTAACAAATGAGAAATGGCACAAACAATTGATGTACGTGCGTCCCTTGATATAAAAAATCAGAAGAATATTGGAAGGTGGCTAACACAAT
400 S Q S S S N N E K W H K Q L M Y W L G S L D K K S E E Y W K V A N T I

1471 TGCAACTGTGCTGAACAACGATGTGAAGCATCGACAAGCAGCTTAAACCTCTGCAATAAAGGAAGGAACGATTGTCAACAAATTCATCAGTACCCTGACAGC
435 A T V L N K R C E A S T S S L N S C N K G K E T I J V N K F I T D L T A

1576 TGGTGGAGTTGAAGTCAGAGTTCTCGAGGTTCCTGGAGAATATTCCAATTTTTCGGATCCTACACITTTTTCGTAAGAAATTCATATGTGAAGTCTGAGTCGGAGGATGT
470 G G V E V R V L E V L E N I P I F G S Y T F A K K F I C E T E S E D V

1681 TCAGAAAGCGCACTCAACGTTATTCTGGCTGGAGCAAGAATTGTATGAACACAACTCACCCACAAGCTCATCAAACTCTTCGCAACACATGCAGCCAGGA
505 Q K A A L N V I L A A S K N L Y E T I Q L T H K L I K L F R N T C S Q E

1786 AACTCCAACTTCTCATCTCAACTCGCCATCGACATCTCTCTCAAAATGTCCTTCAATCATCAAAACGTCGCCACCTTGATCTCTCGCAACTGAGACTCTTAACCC
540 T P T S H S Q L A I D I L L K C V P D H Q N V A T I L I L R T E T L L N P

FIG.4B

1891	CGATGATCAGCAAAATGGCATTACCTGTACAAGGCTATCGAGCGCAAGCGAAACAAGGATGAACCTGAAGCCGAAATTTGGTCGCGAATGCGGAAGTTTAAGGT
575	DDQEKWHYLYKYKAI EASGNKDE LKAEFW SRMRKF KV
1996	TTTCGACCAAACTTCTTGACAGAGCACTTCAGCGGATTCTCATGTTCACTGGCAAGAGATTGCAGATGCTTCAAACCTTCCAACCTGTTCTCCACTGCGAACAC
610	FRPNFLHRLHRA LQA DSHVHWQE IADASNFQLFS TANT
2101	AGAACTTCTGCAAAAATCCTTTAAGAGATCCATCTTTGAGCTATCGATGAAGAAGGGAAGGAGGACACAATTTATTCGCTCCTCCATCGACACTGAGCACCT
645	EFLQKKS FKR SIFELSMKKKG RKEHNLFS L S I D T E H L
2206	TGACCAATTGTGACTGGATCAGCTTCTTCAAGATCCGGCGCTCCACAAAGGTCGTTCGAAATTGGAGTTGCTGGTCACAAGCTACCAACICACCACATCTTCAA
680	EQFVTGSSAS SRS SGA PQGS VRI GVAGHKLP THHIFK
2311	GGGAAGTACTGACCTGCTTCCACTGTCTGGAAGCAGATGGAAGGACCGCATAGGCATTGAAGGTCATGTTCCGTGTTAGAGACGTTGACTATCGGTGCCATT
715	GSTDLLLS T VWEADGR THKA FE GHVPVR DVRLS VPL
2416	GCTCTCTGGATTGACTCTTGACGTTGATAGCGTTGGAGCAATTAGTATGAGAGTTCTTGTCATCGGCGGAAGTTTCCCTTTGGAATCAGAGATCGAATCGAAAGGC
750	LSGLTLLD VDS V G A I S M R V L A S A E V S L W N Q R S N A K A

FIG. 4C

2521 AGAGGCATATACATCGGATCCTTACACCTAACGGCTTCCCTCTACCATCACTCAGAACCCAGTCGCCACGTGGAATCCACAACTCTCGGGCTCTCCACCTTCAC
785 E A Y T S G S L H L T A S L Y H H S E P V R H V E S T I S A L S T F T

2626 CACAGACACCCGTGCAATTTTCGAGACTCTCCCATATGACTTCGCCTAAGAACATCTAATAGCAATGTTGATATCAATCAGAAAACAGTTGTACAGGATCAAAAT
820 T D T R A I F E T L P Y D F C L R T S N S N V D I N Q K T V V Q D Q I

2731 TCGAAAGCATAAAAAGACAGCGCTTAATCGAAAACGAGTACATCCCTGGAGTTACATACAGGTTGGATGACTCGACGATTCGGCAGTGTAAATAGTTATTGGAGCA
855 G K H K K T L N R K R V H P G V T Y R L D D S T I R Q C N S Y L E Q

2836 GTTTAGATTGTAGTTGTTGTTTTTTTTTATTACATTTCATGTTTCTCGGAATCAAAATAAAAAATAACTTATTGAGAAAAAAA
890 F R L *

FIG. 4D

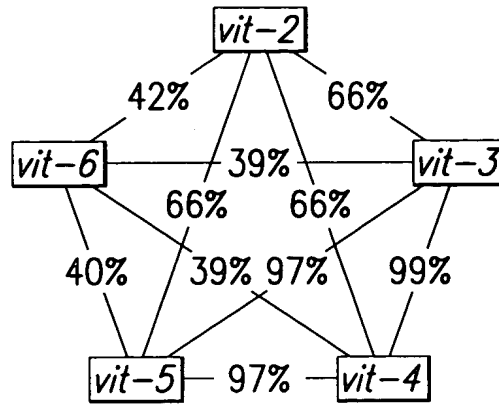


FIG.5A

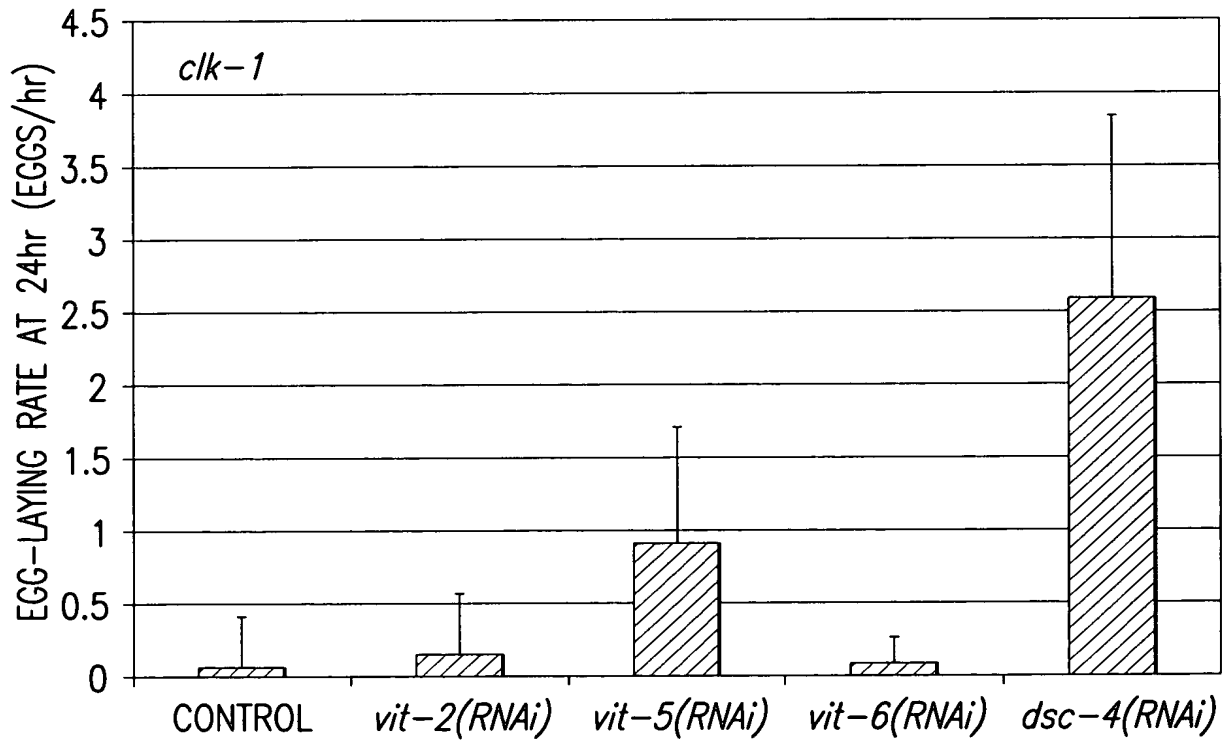


FIG.5B

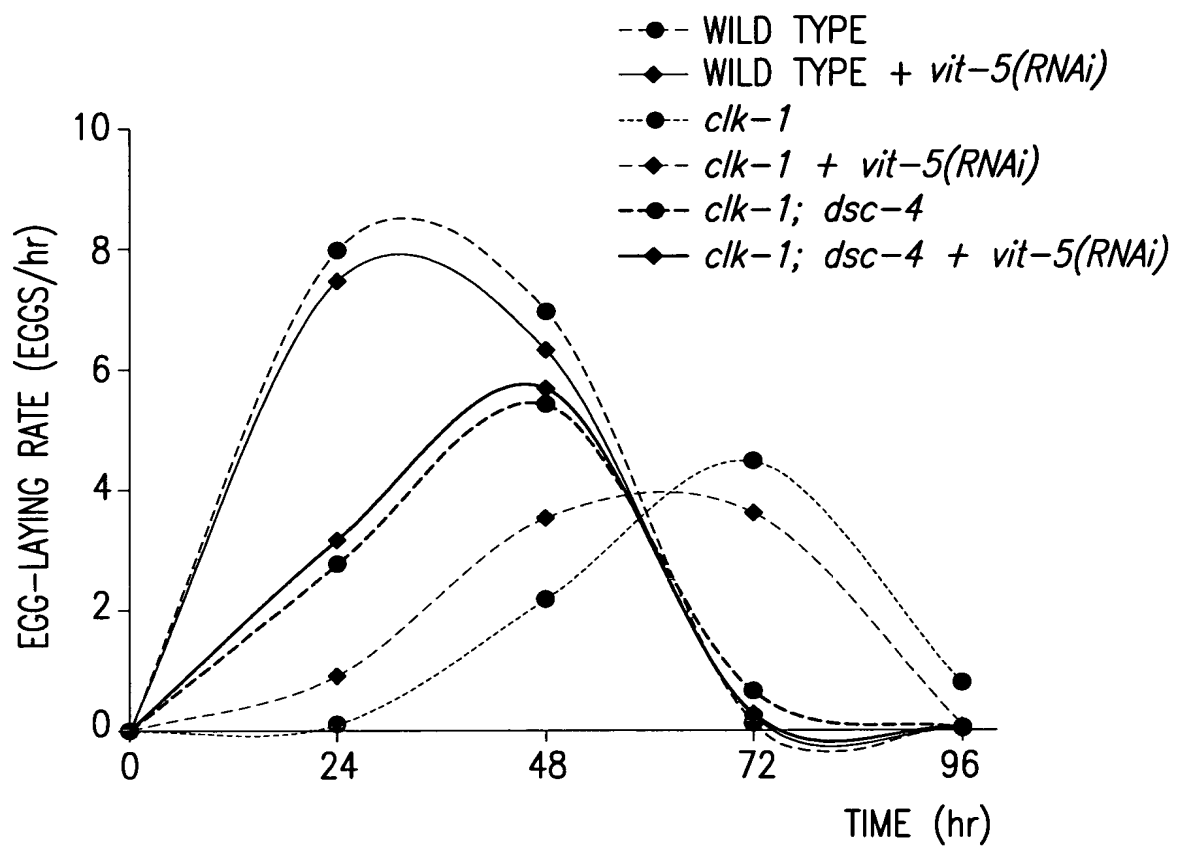


FIG.5C

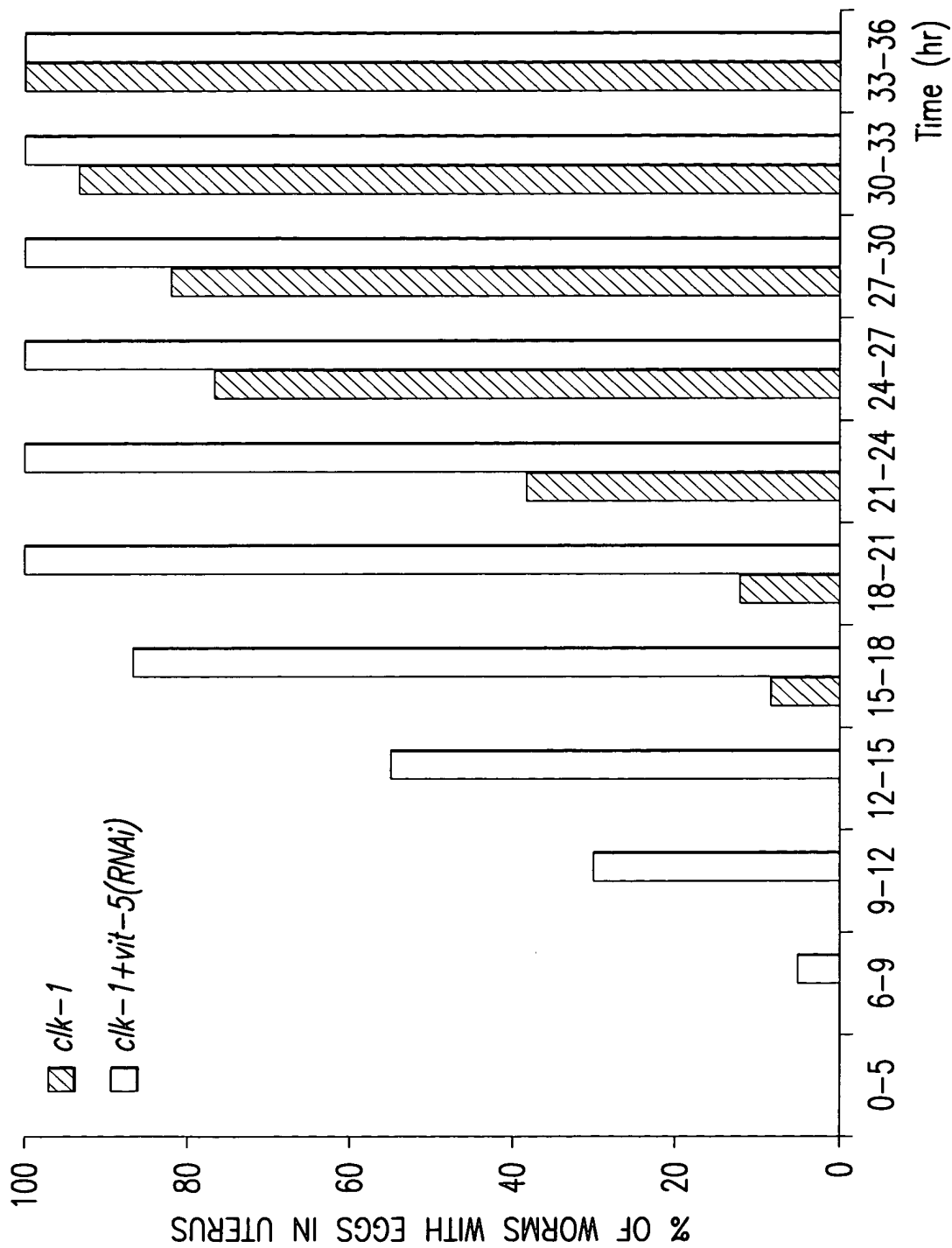


FIG. 5D



FIG.5E

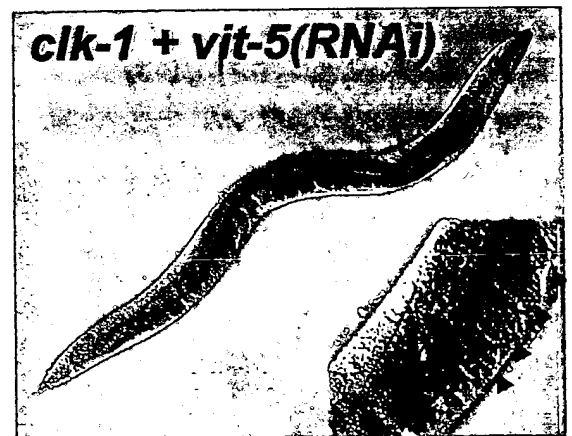


FIG.5F

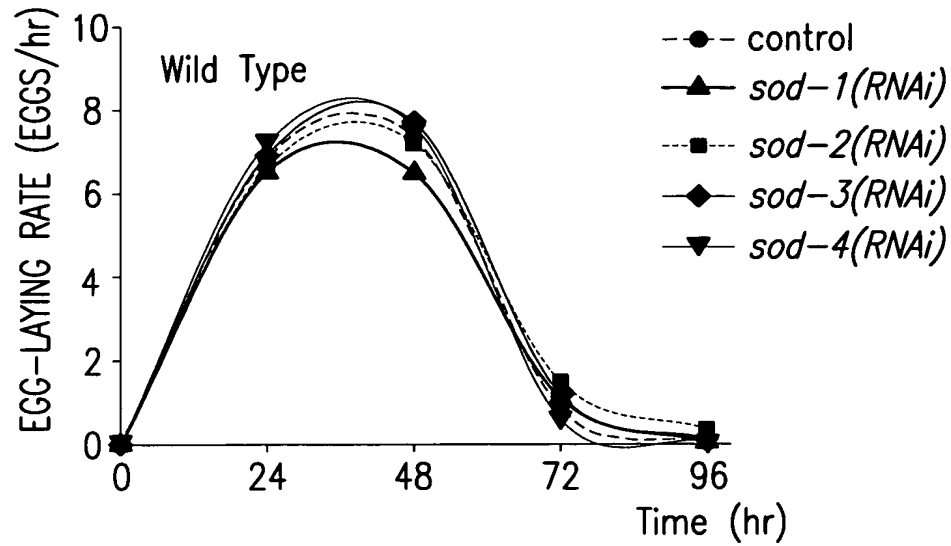


FIG.6A

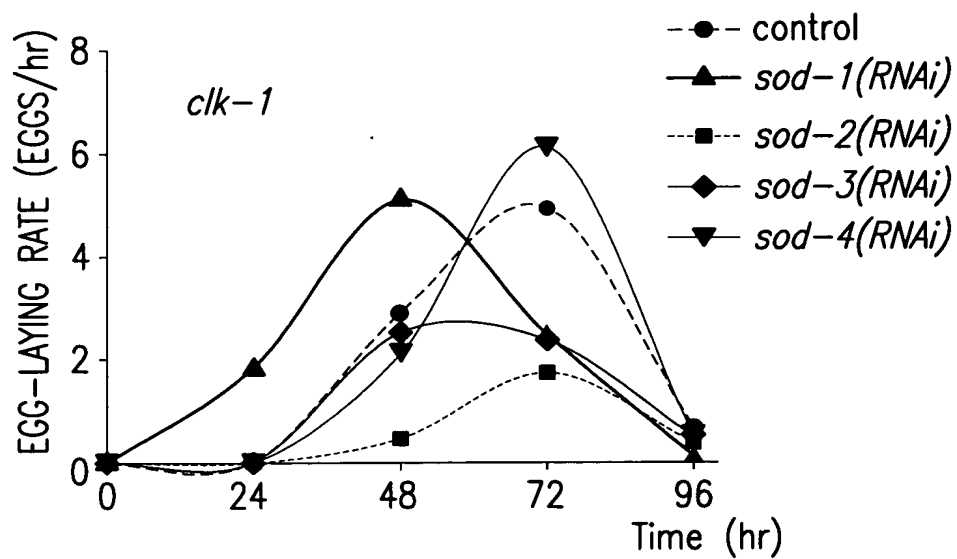


FIG.6B

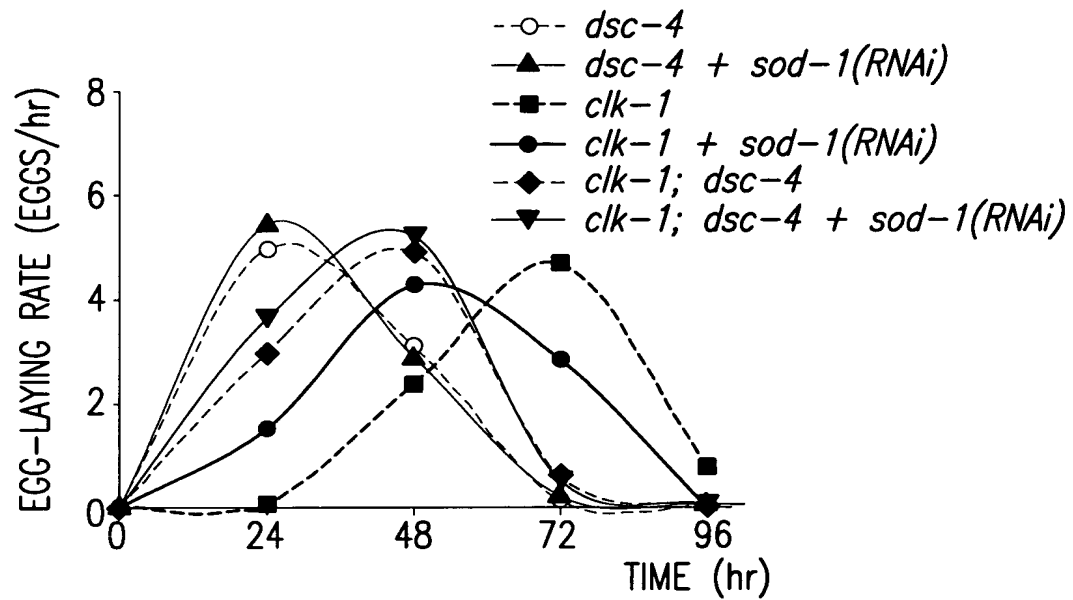


FIG.6C

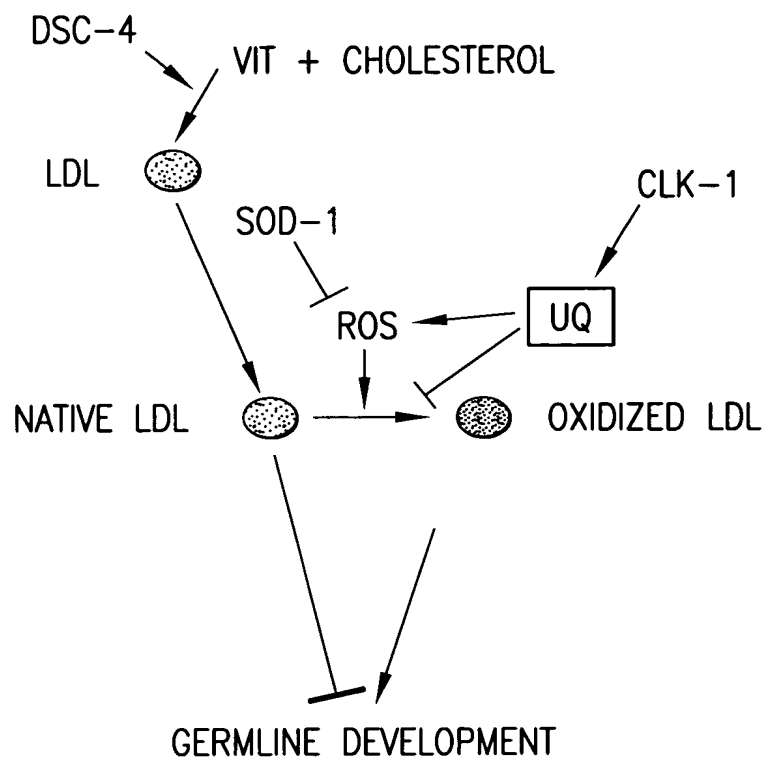


FIG.7A

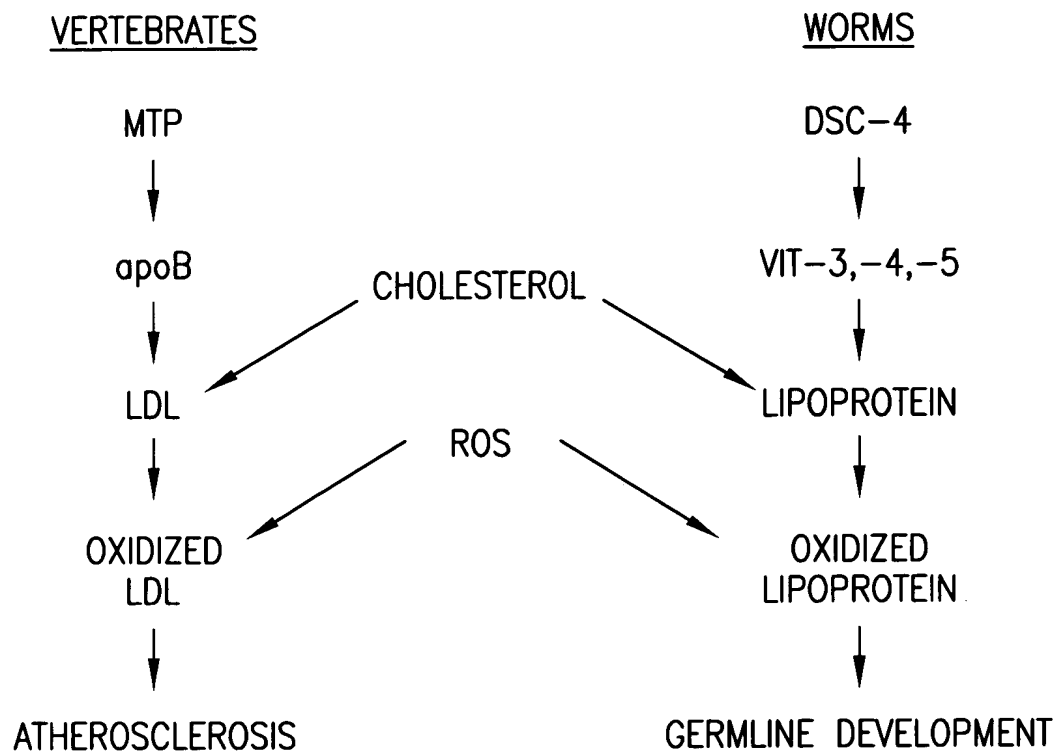


FIG.7B

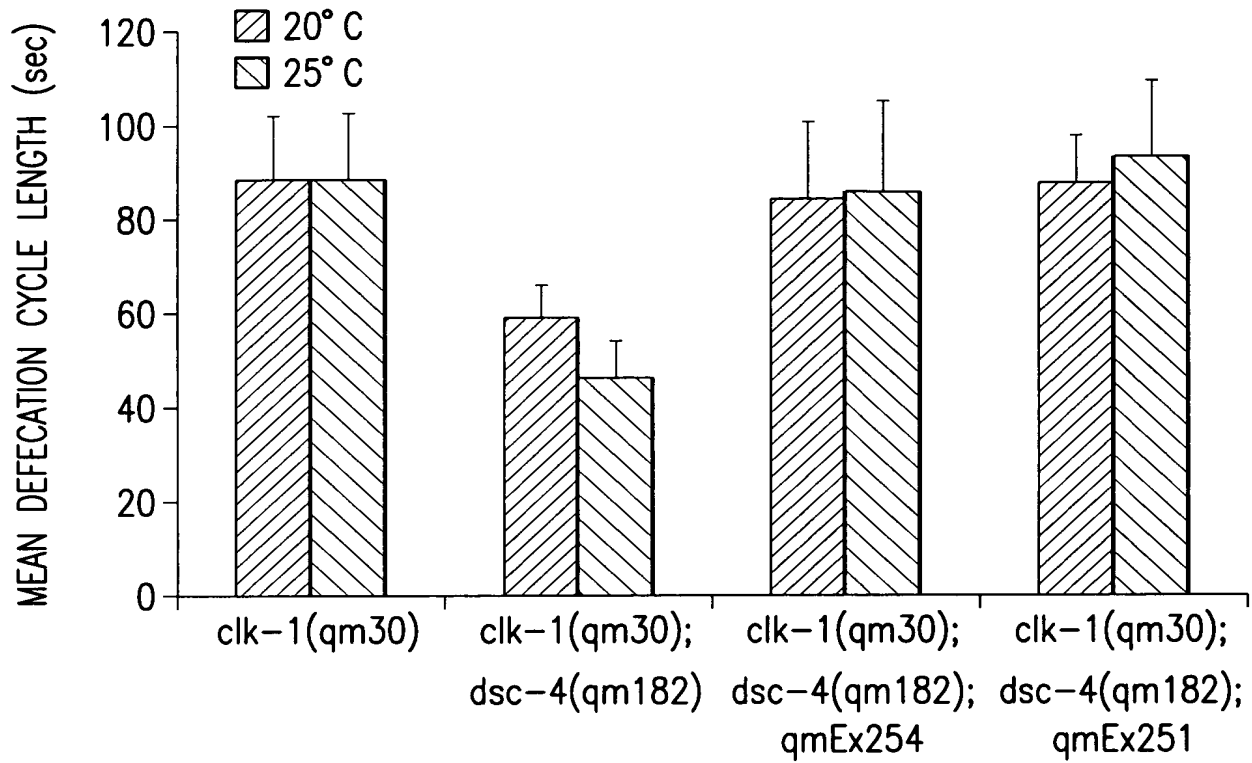


FIG.8A

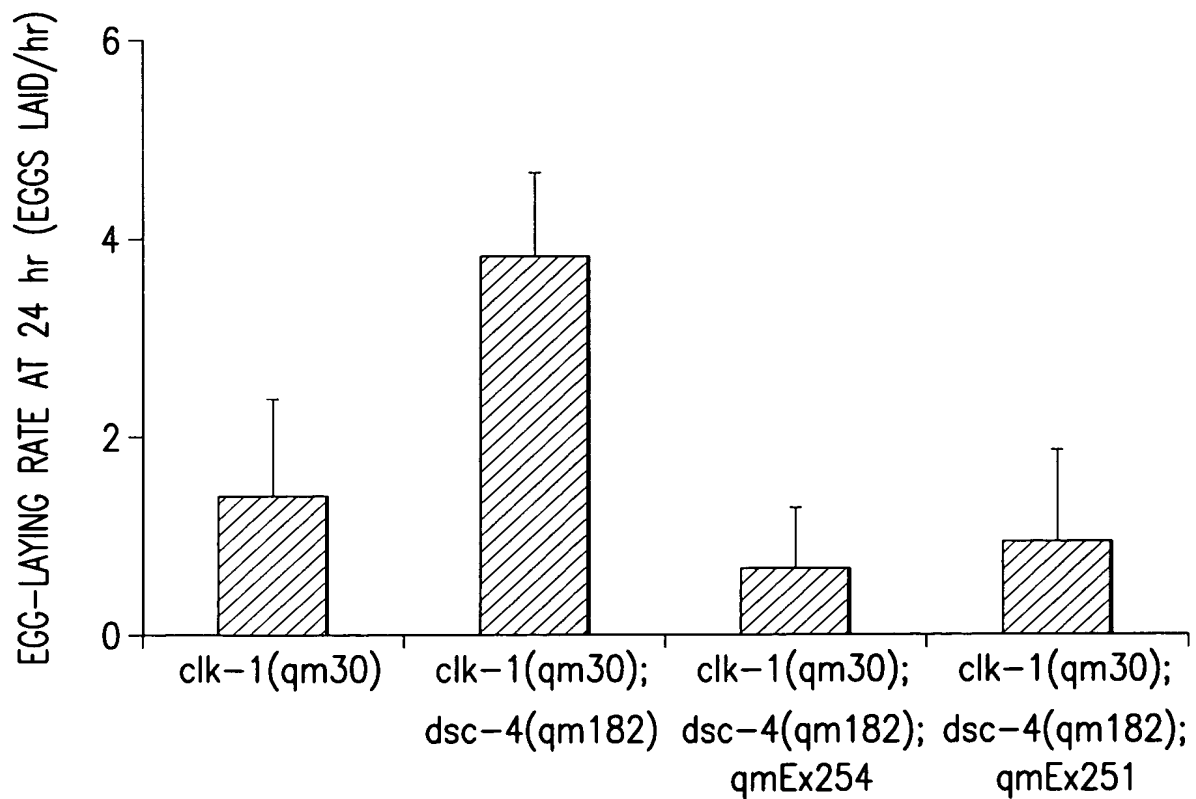


FIG.8B

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1      ATGTTCAAGT GGTGCCATG CTGTTCAAGT ACTTCAAACG AAAAGAATGC GCCGACGGAA
61     CGAAGATTAC GAGCTAACGA TAGGGAATAT AATGCACAAT TCAAATATGC AGACAATGTA
121    ATCAAAACGT CCAAATACAA TATAATCACC TTCATTCTC AAAATTTATT CGAACAATTC
181    CAGCGGATAG CCAACTTTTA TTTTITAGTT TTAATGATAT TACAGTTTAT TCCTCAAATT
241    TCCTCAATTT CCTGGTATTC TACAGCGGTT CCACTGGTTA TTGTATTGGC ATTTTCAGCT
301    ATTAAAGATG GGTACGATGA TGGCAAAGG CACATATCTG ATCGAAATGT AAATGGTCGA
361    AAATCCTACG TAGTTCGAAA TGAAGTCTA TGTGAAGAAG ACTGGAGTAA TGTTAAAGTT
421    GGAGATGTGA TACGAATGAT GAGTAATCAA TTTGTGGCGG CTGATCTTCT ATTATTATCA
481    ACGTCGGAAC CATATGGAGT ATGTTTTATT GAAACTATGG AATTGGATGG AGAAACAAAT
541    CTGAAAAATC GTGCCGCTAT TGCATGTACC CAGGAAATGG GCGACGATTT GGATGGGATT
601    ACGCGCTTTG ATGGAGAAAT AATCTGTGAA CCTCCCAATA ACAACTAGA CAAGTTCAAT
661    GGAAAAATTA TATGAATAA TCATGAATAT GGAGTTAATA ATGATAATAT TCTGCTGAGA
721    GGATGTATTT TGAAGAACAC GAGATGGTGT TATGGAGTTG TCGTTTTTGC TGGAAAAGAT
781    ACAAATTA TGAAGAACAG TGGAAAAACA AAGTTCAAAA GAACGTCTCT CGACCGATTT
841    TTGAATATTT TAATCGTCGG AATTGTGCTT TTTCTCATTG CAATGTGCCT AATTTGTACG
901    ATTTTGTGTG CTGTATGGGA ATATCAAAC TGAAGATATT TTAATTTTA TCTACCGTGG
961    GACGATGTGG TTCCTAGTCC TGAACAAAGA GGTGGCCGCC AAATTGCCCT TATCGCCTTC
1021   CTCCAGTTCT TCTCTACAT CATTCTTCTC AATACAGTTG TACCAATTTT TTTATATGTG
1081   TCTGTGAAA TTATTCGATT TATTCATTCA TTATGGATTA ATTACGACAC TCAAATGTAT
1141   TATGAAAATG GAGAGAAAAG TGTCCACGCA AAGGCACATA CAACAACTTT AAATGAGGAG
1201   TTGGGACAAG TTCAATATGT GTTCAGTGAC AAGACTGGAA CGTTGACAAG GAATATTATG
1261   ACTTTTAATA AGTGTACCAT TAATGGGATC TCGTAACGAG ACATTTATGA TCACAAGGGA
1321   GAGGTTATTG AGACGAATGA CAAAACCAA TCTCTCGACT TTTCTCGAA TTCAGCGTCC
1381   GAACCCACAT TCAAATTTTT CGATAAAAAT CTAGTTGATG CTACAAAACG TCAAGTACCA
1441   GAAATTGATC AATTCTGGAG ACTACTGGCT CTTTGTCTA CTGTAATGCC TGAAAGAGAT
1501   AAAGGACAAC TGGTTTATCA GGCACAATCA CCTGATGAAC ATGCTCTAAC GTCAGCTGCA
1561   AGGAATTTTG GTTATGTTTT CCGAGCAAGA ACGCCTCAA GCATTACGAT TGAAGTGATG
1621   GGAAATGAGG AAATCATGA ATTATTGGCA ATTCTTGATT TTAATAATGA TCGAAAAAGA
1681   ATGCTGTAA TTGTGAAAGG ACCTGATGGA AAGATTGAT TGTATTGTAA AGGCGCTGAT
1741   ATGATGATTA TGCAGAGAAT ACATCCATCA ACATCTCAA TAATGCGTAC CTCAACCAAT
1801   ACTCATCTCG CTGATTTTGC AAATATCGGT CTTGGAACGC TTTGTTTGGG ATACAAGGAT
1861   CTTGATCCAG CGTACTTTTC GGATTGGGAT TCTCGAGTCA AAAAGGCGTC CGCAGCCATG
1921   CAGGACAGAG AATCTGCGGT CGATGCTCTT TACGAAGAAA TTGAAAAAGA TCTGATATTG
1981   ATTGGTGCAA CGGCTATTGA AGACAAGCTT CAGGATGGTG TTCCAGAGGC AATTGCAAGA
2041   CTTTCAGAAG CTAATATCAA GATTTGGGTG CTTACCGGGG ATAAGACAGA AACGGCTATA
2101   AACATTGCCT ACTCGTGTG CCTTCTGACC GATGAAACCA AGGAAATTGT TGATGTTGAT
2161   GGGCAAACG ATACCGAAGT CGAAGTACAG CTAAGAGATA CAAGAAACAC ATTTGAACAG
2221   ATTTTGGCAT TGCCGTCACC GCTTGGAGGA AAGCCACGTA TTGAAATTGA GACAATCCAC
2281   GAGGAGTCCG AGGCTATTTT CTCTGCAAGG AGTATGGATA GAAACATTGT AACTCCTGAT
2341   TTGAAATCAG CAGAAATGGC TGAACACGAG AGTGGAGGTG TTGCTTTGGT AATAAATGGA

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FIG.9A

2401 GATTCATTGG CTTTGGCTCT TGGTCCAAGA CTTGAAAGAA CTTTCTTGA AGTGGCTTGT
2461 ATGTGTAATG CAGTAATATG TTGCGAGTG ACACCACTTC AAAAAGCTCA AGTAGTTGAT
2521 CTAGTAAAC GAAACAAAA AGCAGTGACA CTTTCAATTG GAGACGGAGC AAATGATGTC
2581 AGTATGATCA AGACAGCTCA TATTGGAGTT GGAATTTCTG GCCAAGAAGG AATGCAAGCA
2641 GTATTAGCAT CAGACTATTC AATCGGACAA TTCAAATATC TTGAACGTCT TCTTCTTGT
2701 CACGGTCGAT GGTCTTACAT TCGAATGGCA AAGTTCCTCA GATACTTTT TTACAAAAAC
2761 TTTGCATTTA CACTTACCA CTTCTGGTAT TCATTCTTCT GTGGATATTC TGCTCAAACA
2821 GTTTTTGACG CTGTATTGAT TGCTTGTTAC AATCTCTTT TCACAGCACT TCCTGTTTTG
2881 GCAATGGGAT CTTTGGATCA AGATGTTGAT GATCATTATT CACTGAGATA TCCTAAGCTT
2941 TATCTGCCGG GACAGTTCAA TTTGTTCTT AATATGAGAA TATTTATTTA TTCTGTACTT
3001 CATGGAATGT TTAGTTCCTT TGTGATATTC TTCATTCCAT ATGGTGCATT TTACAACGCA
3061 GCTGCTGCTT CTGGAAGGA TTTGGACGAT TACTCGGCTC TTGCTTTCAC TACTTTTACT
3121 GCATTAGTTG TAGTTGTTAC TGGACAGATA GCCTTCGACA CGAGTTATTG GACGGCAATT
3181 TCGCATTTTG TAATCTGGGG ATCACTTGTT CTGTATTTC TTGTTTGCTT CCTTCTTAC
3241 GAATGGCTTC CAGTTTCATG GATTGTCAAA ACATCATCTT CAATCTCATA TGGTGTGCT
3301 TTTGAACAA TGGTTACTCC TCACTTCTGG TTTTCAATTC TAATGGTTTC AGTTGTACTG
3361 TTACTACCAG TTATGCTTAA TCGATTCTTC TGGCTTGATA CACATCCATC ATTTGCTGAT
3421 AGGCTGAGAA TTCGAAAGAA AATGGGCAAG AAACCATCGG CGAAAGATGA TAAAAAACC
3481 GCATTCAAAC GCACGGCAGC AACTCGACGA AGTGTCCTG GATCACTTAG AAGTGGTTAC
3541 GCATTCTCTC ATTCACAAGG ATTCGGAGAA CTCATTCTCA AAGGAAAATT GTTCAAAAAT
3601 GTGGAAAATC TACGGGGAAA GAATAATTG AATGCGAAAA TTCACCCGAC TTCTGATGAC
3661 TTGCAGCCGA TGCTTATTC TAGTGTGCTT GATGACAGCC AAGGAGCTTC AAGTATTAAT
3721 GCAATGCACC TTCCAATGGG TACAGTCCA CAGAATGTAC CCCATACATT GAATGTAAAT
3781 ACTGATGACT GGTCTCAATC ATCGGATTTT CGTCCAGCCT ATGCAAAGGA ACCATCACCA
3841 CTGCAGGGTA CAGTAATCCG TGGCGATGGA CGGAGCCATA GAAACCACGT GTATTGCGG
3901 GAAACTCAGG TGAAGAACA ACCAGACGTA ATCACTCGCC TTAA

FIG.9B

1 MFSWLPCCSS TSNEKNAPTE RRLRANDREY NAQKYADNV IKTSKYNIIIT FIPQNLFEQF
61 QRIANFYFLV LMILQFIPQI SSISWYSTAV PLVIVLAFSA IKDGYDDAQR HISDRNVNGR
121 KSYVVRNGSL CEEDWSNVKV GDVIRMSNQ FVAADLLLLS TSEPYGVCFI ETMELDGETN
181 LKNRAAIACI QEMGDDLDGI TRFDGEIICE PPNNKLDKFN GKLIWNHEY GVNNDNILLR
241 GCILKNTRWC YGVVVFAGKD TKLMMNSGKT KFKRTSLDRF LNILIVGIVL FLIAMCLICT
301 ILCVWEYQT GRYFTIYLPW DDVPSPEQR GGRQIALIAF LQFFSYIILL NTWPISLYV
361 SVEIIRFIHS LWINYDTQMY YENGESVPA KAHTTILNEE LGQVQVFSK KTGTLIRNIM
421 TFNKCTINGI SYGDIYDHKG EVIETNDKTK SLDFSWSNAS EPTFKFFDKN LVDATKRQVP
481 EIDQFWRLLA LCHTVMPERD KGQLVYQAQS PDEHALTSAA RNFGYVFRAR TPQSITIEVM
541 GNEETHELLA ILDFNNDKR MSVIVKPGDG KIRLYCKGAD MMIMQRIHPS TSQIMRTSTN
601 THLADFANIG LRTLCLGYKD LDPAYFSDWD SRVKKASAAM QDRESAVDAL YEEIEKDLIL
661 IGATAIEDKL QDGVPEAIAR LSEANIKIWW LTGDKTETAI NIAYSCRLLT DETKEIVVVD
721 GQDTEVEVQ LKDTNRNTEFQ ILALPSPLGG KPRIEIEIHH EESEATSSAR SMDRNIVTPD
781 LKSAEMAEHE SGGVALVING DSLAFALGPR LERTFLEVAC MCNAVICCRV TPLQKAQVVD
841 LVKRNNKAVT LSIGDGANDV SMIKTAHIGV GISGQEGMQA VLASDYSIGQ FKYLERLLLV
901 HGRWSYIRMA KFLRYFFYKN FAFTLTNFWY SFFCGYSAQT VFDAVLIACY NLFFTALPVL
961 AMGSLDQDQD DHYSLRYPKL YLPGQFNLF NMRIFIYSVL HGMFSSLVIF FIPYGAFYNA
1021 AAASGKDLD YSALAFITFT ALVVVVTGQI AFDTSYWTAI SHFVIWGSVL LYFLVCFLY
1081 EWLPVSWIVK TSSISYGVA FRTMVTPHFW FSILMVSVL LLPVMLNRFF WLDTHPSFAD
1141 RLRIRKKMGK KPSAKDDKKT AFKRTAATR SVRGLRSYG AFSHSQGFE LILKGKLFKN
1201 VENLRGKNNS NAKIHPTSD LQPMLISSVP DDSQGASSIN AMHLPMTGTRP QNVPHTLNVN
1261 TDDWSQSSDF RPAYAKEPSP LQGTVIRGDC RSHRNHVYSR ETQVEEQPDV ITRL*

FIG. 10

H06H21.10a	0
ATP8B1	0
ATP8B2	0
ATP8B3	MGHHPAASSASRTVGGVPSVWSWALCTELASLSALPRDRDCTQMDRWHRANGSTTSAALDARGLPPASPAPT	75
ATP8B4	0
Consensus		
H06H21.10a	0
ATP8B1	0
ATP8B2	0
ATP8B3	RSTRACPEPSPAPPGDTCGSDVTQECGCPAGIRGVEKIPGSSDDVRLPPSPPEFAAQPGVGCGPRQDTQPM	150
ATP8B4	0
Consensus		
H06H21.10aMFSWLPCCSSTSNEKNAPT	19
ATP8B1	MSTERDSETTFDEDSQPNDDEVVPYSDDETEDELDDQGSAVEPEQNRVNREAEENREFRKECTWQVKANDRKYHE	75
ATP8B2MDTLRAVPLFSISGLFSFPYRVSHG IAGILLGEMAVCAKKRPPEE	45
ATP8B3	AGHSEPGGEAADDECGSPTSMGSLGQREDLQDEDRNSAF.....TWKVQANNRAYNG	199
ATP8B4	0
Consensus		
H06H21.10a	ERRLRANDREYNAQFKYADNVIKTSKYNIIITFIPQNLFEQFQRIANFYFLVLMILQFIPQISSISWYSTAVPLVI	94
ATP8B1	QPHFMTKFLCIKESKYANNAIKTYKYNATFIPMNLFEQFKRAANLYFLALLILQAVPQISTLAWYTTLLVPLLLV	75
ATP8B2	ERRARANDREYNEKFQYASNCIKTSKYNILTFLPVNLFEQFQEVANTYFLFLLILQLIPQISSLSWFTTIVPLVL	120
ATP8B3	QFKEKVI..LCWQRKKYKTNVIRTAKNFYSFPLPLNLYEQFHRVSNLFFLIIILQSIPDISILPWFSLSTPWC	274
ATP8B4	0
Consensus		

FIG. 11A

H06H21.10a	VLAFAIKDGYYDAQRHISDRNVNCRKSYVVRNGSLCEEDWSNVKVGIVIRMSNQFVAADLLELLSTSEPGYGVQF	169
ATP8B1	VLGVTAIKDLVDDVARHKMDKEINNRTICEVIKDGRFKVAKWKEIQVGDIVRLKKNDFAADLLELLSSSEPNLSLEY	225
ATP8B2	VLTTITAVKDATDDYFRHKSDNQVNNRQSQVLINGILQQEQMNVVCVGDIIKLENNQFVAADLLELLSSSEPHGLLEY	194
ATP8B3	LLFIRATRDLVDDMGRHKSDRAINNRPQCILMGKSKQKKWQDLCVGDVVCLRKDNIAPADMMLELASTEPSSLEY	349
ATP8B4MNVKVGDIIKLENNQFVAADLLELLSSSEPHGLLEY	34
Consensus	vgd v ad lll ep c	
H06H21.10a	IEIMELDGEINLKNRAAIACTQEMGDDLDGITREDDGEIICPEPANKLDKENQKLIWNNHEYGVNNDNILEPCCIL	244
ATP8B1	VEIAELDGEINLKFKMSLEIADQYLQREDTLATDDGEIECEEPANRLDKEIGTETFWRNTSFPLDADKILEPCCVI	300
ATP8B2	ITIAELDGEINLKNVRQAIPVASELGDISKLAKEDGEVIECEPANKLDKESGTEYWKENKFPLSNQNMILEPCCVL	269
ATP8B3	VEITVIDDGEINLKFQALMVTHKELATIKKMASQGTVTCEAPNSRMHHEVGCCEWNDKKYSLDIGNILLEPCCRI	424
ATP8B4	VEIAELDGEINLKNVRHALSVASELGADISRLAGDDIVVCEVPANKLDKEMGTEISWKDSKHSLNNEKILEPCCIL	109
Consensus	et dgetn k t f g ce pn f g l w lrgc	
H06H21.10a	KNTRWGCGVAVFAGKDTKLMMNSCKTKFKRTSLDRFLKILIVGVLFILAMCLICTILCAVWEYQYQTRYFTIYLP	319
ATP8B1	RNTDECHGLYIFAGADTKIMKNSCKTRFKRTKIDYLMYMYVTIFVVLILLSAGLAIGHAYWEAQVGNSSWLYLD	375
ATP8B2	RNTIEWCFGLYIFAGPDTKLQNSGRTKFKRTSIDRLMXTLVLWFFGFLVCMGVILAIGNAIVEHEVGMRFQVYLP	344
ATP8B3	RNTDTGCGLYIYAGFDTKIMKNCCKIHLKRTKLDLLMCKLVVVFISVVLVCLVLAFGCGFSVKEFKDHHYLLSG	499
ATP8B4	RNTSMWCFGMVIFAGPDTKLQNSCKTKFKRTSIDRLMXTLVLWFFGFLICLGIILAIGNSIWESQTGDQFRTFLF	184
Consensus	nt c g v ag dtk m n g krt d n i	
H06H21.10a	WDDVVPSEQRGGRQIALIAFLQFFSYIILLNTVPISLYVSVEIRFIHSLWINYDTQMYYENGEKSPAKAHT	394
ATP8B1	GEDDTPSYR..G.....FLIFWGYIIVLNTMVPISLYVSVEIRLGGSHFINWDLQMYYEAKDT..PAKART	438
ATP8B2	WDEAVDSAFFSG.....FLSFWSYIILLNTVPISLYVSVEIRLGHSYFINWDKMFCKMKRT..PAEART	409
ATP8B3	VHGSSVAAESFFVWSFLILLSVTIPMSMFIILSEFIYLGNSVFIIDWDVQMYKPDQVPAKARSTSLNDHLGQVEY	574
ATP8B4	WNEGEKSSVFSG.....FLTFWSYIILLNTVPISLYVSVEIRLGHSYFINWDRKMYYSRKAII..PAVART	249
Consensus		

FIG.11B

H06H21.10a	TTLNEELGQVQYVFS	SDKTGTL	TRNIMTFN	KCTING	ISYGD	IYDH	KGEV	ETND	TKSL	DFS	WNS	ASEPT	IF	KE	FDK	469
ATP8B1	TTLNEQLQGIHYIF	SDKTGTL	TQIMTFK	KCCING	QIYGD	HRD	ASQ	HNK	IEQ...	VDFS	WNT	YAD	GK	LA	EYDH	513
ATP8B2	TTLNEELGQVEYIF	SDKTGTL	TQIMVFN	KCSING	SHSYGD	VDV	LGH	KAE	LGER	PEPV	VDFS	NPL	AD	KFL	EWD	484
ATP8B3	IFSDKTGTL	TQNIL	TFN	KCCIS	GRV	GP	DEAT	TR	KEN	PYL	WNKF	AD	GK	LL	E	630
ATP8B4	TTLNEELGQIEYIF	SDKTGTL	TQIMTFK	RCSING	RIYGE	VHDD	L	DQ	KE	IT	QEK	EP	VDFS	VKS	QAD	324
Consensus																f
H06H21.10a	NEVDAT	KQVPE	IDQF	WRL	ZAL	CH	T	V	M	P	R	D	K	G	Q...	538
ATP8B1	Y Z	IEQ	IS	G	KE	P	E	V	R	Q	F	F	L	A	V	580
ATP8B2	S Z	LEAV	K	I	G	D	P	H	T	H	E	.	F	F	R	554
ATP8B3	A Z	LHL	V	R	T	N	G	D	E	A	V	R	E	F	W	704
ATP8B4	H Z	M	E	S	I	K	M	G	P	K	V	H	E	.	F	394
Consensus																t
H06H21.10a	VMGNEE	THE	L	A	I	L	D	E	N	D	R	K	R	M	S	601
ATP8B1	ELG	T	E	R	T	Y	N	V	L	A	I	L	D	E	N	645
ATP8B2	EMG	T	A	I	T	Y	Q	L	L	A	I	L	D	E	N	619
ATP8B3	ELG	E	E	R	V	Y	Q	L	L	A	I	L	D	E	N	779
ATP8B4	ELG	T	L	V	T	Y	Q	L	L	A	I	L	D	E	N	459
Consensus																t
H06H21.10a	HLADF	AN	I	G	L	E	R	T	L	C	L	G	Y	K	D	658
ATP8B1	FANET	...	L	R	T	L	C	L	G	Y	K	E	I	E	E	698
ATP8B2	HLNE	Y	A	G	E	L	R	T	L	C	L	D	E	E	Y	673
ATP8B3	VRRN	G	R	L	Q	P	G	M	A	M	Y	E	A	F	A	850
ATP8B4	HLSE	F	A	G	E	L	R	T	L	C	L	G	Y	K	E	513
Consensus																e

FIG.11C

H06H21.10a	IÉLGATAIÉDQKQDQVPEAIARÉSEANIKIHWLTGDKT.....	ÉTAIINIAYSQRLÉTDEIKEI	716
ATP8B1	IÉLGATAIÉDQKQDQVPEITISKÉAKADIKIHWLTGDKK.....	ÉTAENIGFACÉLÉTEDTTIC	756
ATP8B2	MÉLGATAIÉDQKQDQVPEITIALÉTLANIKIHWLTGDKQ.....	ÉTAVNI GYSQKMLTDDMTEV	731
ATP8B3	RÉLGATAIÉDRLQDQVPEITIKÉKKSNIKIHWLTGDKQSQCGAGRRGAELVCFAE.....	ÉTAVNI GFAÉLÉSENMLIL	925
ATP8B4	MÉLGATAVÉDQKQDQVPEITVTSÉSIANIKIHWLTGDKQ.....	ÉTAIINI GYAQNMÉTDDMNDV	571
Consensus	l gata ed lg gv e l ikiwvltgdk	eta ni c l	
H06H21.10a	VWDGQTDTEVEVQLKDRNTFEQILALPSLPGKPRIEIETIHEESEAISSARSMDRNIVTPDLKSAEMAHEHS		791
ATP8B1	YGEDINSLHARMENQNRGGVYAKFAPPVQESFFPPGGNRALITGSWLNEILLEKTKRNKIL.....		821
ATP8B2	FIVTGHTVLEVREELRKAREKMDSSRSV.....	GNGFTYQDKLSSSKLTSVLEAVAGE.Y.....	786
ATP8B3	EEKEISRILETYWENSNNLLTRESLSQVKLALVINGDFLDKLLVSLRKEPRALAQNVNMEDAWQELGQSRDRFLY		1000
ATP8B4	FVIAGNNAVEVREELRKAKQNLFGQNRNF.....	SNGHVCEKKQQLDLSIVEETITGDY.....	627
Consensus			
H06H21.10a	GGVALVINGDSLAFALGPRIERTFLEV.....	ÁCMQNAVITCCRVTPQLQKAQVVDLÁVRNKKAVTÉSL	853
ATP8B1	...KLKFPRTEEERRMRTQSKRRLEAKKEQRQKN..FVDLÁCEQSAVITCCRVTPKQKAMVVDLÁVRKKAITÉAL		891
ATP8B2	...ALVINGHSLAHALEADMELEFLET.....	ÁCAQKAVITCCRVTPQLQKAQVVDLÁVRKKAITÉAL	845
ATP8B3	ARRLSLLCRRFGLPAAPPAQDSRRRSSEVLQERAFVDLÁSKQQA VITCCRVTPKQKALIVALEÁVRKYHQVWÉAL		1075
ATP8B4	...ALVINGHSLAHALESDVKNDLLEL.....	ÁCMQKTVITCCRVTPQLQKAQVVDLÁVRKKAITÉAL	686
Consensus		a c vicervtp qka v lvk t l i	
H06H21.10a	QDQANDVSMKKTAHICVQGISQDQEQMCAVLA SQYSIGQFKYERLLLVHGRWSYIRMAKFLRYFFYKNFAFTLTINF		928
ATP8B1	QDQANDVNMKKTAHICVQGISQDQEQMCAVMSQYSFAQRYÉQRLLLVHGRWSYIRMKKFLRYFFYKNFAFTLVHF		966
ATP8B2	QDQANDVSMKKTAHICVQGISQDQEQIQAVLASQYSFSQFKÉQRLLLVHGRWSYLRMKKFLCYFFYKNFAFTMVHF		920
ATP8B3	QDQANDINMKKTADVQVSLAGQDQEQMCAVQN SDFVLGQFCFÉQRLLLVHGRWSYVRICKFLRYFFYKSMASMMVQV		1150
ATP8B4	QDQANDVSMKKS AHICVQGISQDQEQLQAVLASQYSFAQRYÉQRLLLVHGRWSYFIRMKKFLCYFFYKNFAFTLVHF		761
Consensus	gdgand mik a gvg ggeg qav sd qf l rlllvhgrwsy r kfl yffyk a		

FIG.11D

H06H21.10a	WYSFFCQYSAQ TVF DAVLIACYN WLF FTAL PVW AM SLDQD DDHY SL RY P K EL LP CG FN LF FM MRIF IYSVL HGM	1003
ATP8B1	WYSFFNQYSAQ TAYEDWFI TL Y W VL YT SL PV EL M LL DQD YSDKL SL RF P GL Y IV GG RDLL FN YKRFFVSLL HGV	1041
ATP8B2	WFGFFCQYSAQ TVYDQYFI TL Y W IV YT SL PV EL M LL DQD YPEQR SM EY P K EL PE CG FN LF FM KREFFICIAQ Q I	995
ATP8B3	W FACYN Q FTG Q PL YEGWFLAL F LL YT SL PV EL M LL DQD YSAEQ SL EK P EL YV GG Q DEL FN YWV F VQAI AHGV	1225
ATP8B4	WFGFFCQYSAQ TVYDQWFI TL Y W IV YT SL PV EL M LL DQD YSDQN SV DCPQ Y K P CG FN LL LF FM KRKFFICVL HGI	836
Consensus	w g q n l p v l g q d v s p l y g q f n f g	
H06H21.10a	F S SLV I FF IP YCAFYNAAAASGKDLD D YSAL A FTTFTALV..VVTGQIAFDTS Y WTAISHFVIWGSLLVLYFLVC	1076
ATP8B1	L T SMIL FF IP L GCAYLQTVGDGEAPSD Y QSF A VTIASALV..ITVNGQICLDT S WTFVNAFSIFGSI AL YFGIM	1114
ATP8B2	Y T SVLM FF IP Y GVFADATRDDGTQLA D YQSF A VTVATSLV..I V SVQICGLDT G WTA I NHFFIWGS L AVYFAIL	1068
ATP8B3	T T SLVN FF MTLWISRD T AGPASF..S D HQSF A VVVALSCLLSIT M EVGKVLTPSPWTW P MEASSPGDPCF G GIA	1298
ATP8B4	Y T SLVL FF IP Y CAFYNVAGEDCQ H IA D YQSF A VTMTATSLV..I V SVQIALDT S WTF I NHVFIWGS I AIYFSIL	909
Consensus	s f f d a	
H06H21.10a	FLLYE W LPVSWIVKTS SI SYGVAFTMTWTPHF W FSILM V SV V LLLPV M LNR F FWLDTHP S FADRLRIRK K MGKK	1151
ATP8B1	FDFHSAGI H VLFP S AFQ IG TASNALRQ P YIWL I ILTV..AVCLLPV V AIR F LSMTIWP S ESDKIQKH...RKR	1184
ATP8B2	FAMHSNGLFDM F PNQ FR VGNAQNTLAQ P TVWL T IVLT..VVCIMPV V AFR F LRLNLKPDLS D TVRYTQLVR K K	1141
ATP8B3	RCPSWTPGAGVLVQAPLGP G FTPPLPVQ V ILIIKYWTALCVATILLSLG F YAIMTTT T TSQSWLFRVSP T TFPFL.	1372
ATP8B4	FTMHSNGIFGIFPNQ FP VGNARHSLTQKCIWL V ILLTT..VASVMPV V AFR F LKV D LYPTLS D QIRRWQAQ K K	982
Consensus		
H06H21.10a	PSAKDDKKTAFKRTAAT...RRSV R GSLRSGYAFSHSQGF G ELILKGKLFKNVENLRGKNNSNAKIHPTSD D LQP	1223
ATP8B1	LKAEQWQRRQ Q VFRRGVSTR R RSAYAFSHQ R G Y ADLISSGRSI.....RKKRSP	1233
ATP8B2	QKAQHRCMR R VGR T GS...RRSGYAFSHQEGF G ELIMSGKNMRLSSLALSSF T TRSS...SWIESLR R KKSDS	1209
ATP8B3YADLSVMSSPSILLVLLSVSINTFPV L ALRVIFPALKELRAK	1415
ATP8B4	ARPPSSRRPR T RRSS...RRSGYAF A HQEGY G ELITSGKNMRAKNPPPTSGLEKTHYNSTSWIENLCK K TTDT	1053
Consensus		

FIG.11E

H06H21.10a	MLISSVPDDSQGASSINAMHLPMGTRPQNVPHTLNVNTDDWSQSSDFRPAYAKEPSPLQGTVIRGDCGRSHRNHVY	1298
ATP8B1	LDAIVADGTAEYRRTCDS	1251
ATP8B2	ASSPSGGADKPLKG	1223
ATP8B3	EEKVEEGPSEEIFTMEPLPHVHRESRARRSSYAFSHREGYANLITQGTILRRGPGVSSDIASESLDPSDEEAASS	1490
ATP8B4	VSSFSQDKTVKL	1065
Consensus		
H06H21.10a	SRETQVEEQPDVITRL	1314
ATP8B1		1251
ATP8B2		1223
ATP8B3	PKESQ	1495
ATP8B4		1065
Consensus		

FIG. 11F